

SEQUENCE LISTING

<110> Young, Karen K. Y.

<120> Compositions and Methods for Detecting Certain
Flaviviruses, Including Members of the Japanese
Encephalitis Virus Serogroup

<130> 022101-000230US

<140> US 10/815,480

<141> 2004-03-31

<150> US 60/459,491

<151> 2003-03-31

<150> US 60/552,454

<151> 2004-03-12

<150> US 60/555,530

<151> 2004-03-22

<160> 919

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 gwaascnsy crramcysyy tcggrw 26

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 gaaascnct crraacygty tcggaa 26

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 <223> Koutango virus Primer 1, region of conserved
 sequence in 3' untranslated region of the genome
 of Japanese encephalitis virus serogroup, KY1129

<400> 7
 gtaagccctc agaaccgtct cggaa 25

<210> 8
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 <212> DNA
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 serogroup amplification primer

<400> 8
 gtaagccctc agaaccgtct cggaa 25

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<220>
 <223> region of conserved sequence in 3' untranslated
 region of the genomes of flaviviruses, consensus
 sequence

<400> 9
 tctcctagtc tatcccaggt gtcaa 25

<210> 10
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 <213> Artificial Sequence

<220>
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 agaggatcag ataggggtcca cagtt 25

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<220>
 <223> Japanese encephalitis virus serogroup Primer 2

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<400> 11
 yccyastmtw nyccaggtr tcaa 24

<210> 12
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 ycctagtcta tcccaggtrt caa 23

 <210> 13
 <211> 24
 <212> DNA
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 <223> Japanese encephalitis virus Primer 2

 <400> 13
 cccyastmta tyyccagggtg tcaa 24

 <210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Murray Valley encephalitis virus Primer 2

 <400> 14
 tcctagtctt ttcccagggtg tcaa 24

 <210> 15
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 <212> DNA
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 amplification primer, region of conserved sequence in 3'
 untranslated region of the genome of Japanese encephalitis
 virus serogroup, KY1129

 <400> 15
 tcctagtcta tcccagggtgt caa 23

 <210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of flaviviruses, KY1129

 <400> 16
 ggactagagg ttagaggaga ccccgcg 28

 <210> 17
 <211> 28
 <212> DNA
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 <223> complement to SEQ ID NO:16

<400> 17
 ccgcgggggtc tcctctaacc tctagtcc 28

<210> 18
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe for detecting flaviviruses, oligonucleotide
 that hybridizes to conserved region of flaviviral
 nucleic acid

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 <222> (25)...(25)
 <223> n = g, c, t, a or absent

<220>
 <221> modified_base
 <222> (26)...(26)
 <223> n = c, t, g or absent

<220>
 <221> modified_base
 <222> (27)...(28)
 <223> n = g, c, a, t or absent

<400> 18
 ggwctagwgg ttagaggaga ccynnnnn 28

<210> 19
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe for detecting Japanese encephalitis virus
 serogroup members

<400> 19
 ggactagwgg ttagaggaga ccccrykk 28

<210> 20
 <211> 28
 <212> DNA
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<220>
 <223> probe for detecting West Nile virus

<400> 20
 ggactagwgg ttagaggaga cccrcgk 28

<210> 21
 <211> 28
 <212> DNA
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<220>
 <223> probe for detecting Japanese encephalitis virus

<400> 21
 ggactagagg ttagaggaga ccccgygg 28

 <210> 22
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 <212> DNA
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 <220>
 <223> probe for detecting Murray Valley encephalitis virus

 <400> 22
 ggactagagg ttagaggaga ccccactc 28

 <210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe for detecting Kunjin virus

 <400> 23
 aataygtgga ttacatgast tcaytgaag 29

 <210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe for detecting Dengue virus

 <400> 24
 ggactagagg ttagaggaga ccccyssv 28

 <210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe for detecting yellow fever virus

 <400> 25
 ggtctagagg ttagaggaga ccctccag 28

 <210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe for detecting Montana myotis
 leukencephalitis virus

 <400> 26
 ggactagagg ttagaggaga ccccttcc 28

<210> 27
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> probe for detecting Modoc virus

<400> 27
 ggactagagg ttgagggaga cccccggc 28

<210> 28
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Example Probe 1, Japanese encephalitis virus
 serogroup amplification primer

<400> 28
 ggactagagg ttagaggaga cccccggg 28

<210> 29
 <211> 418
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate BFS1750

<400> 29
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtta 60
 tcaaagccaa tctggccgag tgcaaagccc ctcatccga ctcgaggagg tccctagcac 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
 ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 30
 <211> 342
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate 1750-Std

<400> 30
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtta 60
 tcaaagccaa tctggccgag tgcaaagccc ctcatccga ctcgaggagg tccctagcac 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
 tggcaaggcc caaaccgct cgaagctgta gagacgggg aa 342

<210> 31
 <211> 418
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate TD6-4G

<400> 31
 ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
 tcaaagccaa tctggccgag tgcaaagccc ctcatgccga ctcgaggagg tccctggcac 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgcaac 300
 tcggcaaggc ccaaaccgcg tcgaagctgt agagatgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 32
 <211> 342
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate CoaV750

<400> 32
 ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
 ccaaagccaa tctggctgag tgcaaagccc ctcggtccga ttcgggaggg tccctggcac 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgcgcaact 300
 tggcaaggcc aaaaccgcgt cgaagctgta gagatggggg aa 342

<210> 33
 <211> 418
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate L695121.05

<400> 33
 ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
 tcaaagccaa tccggctggg tgcaaagccc ctcatgccga ctcgaggagg tccctggcat 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgccca cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
 ttggcaaggc ccaaaccgcg tcgaagctgt agagacgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 34
 <211> 418
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate TNM771K

<220>
 <221> modified_base
 <222> (384)...(384)
 <223> n = g, a, c or t

<400> 34
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccagggt gactgggtca 60
 tcaaagccaa tctggctggg tgcaaagccc ctcatccga ctcgaggagg tccctggcac 120
 gtaggctgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
 gctgtctgta catgcccac gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag agcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
 ttggcaaggc ccaaaccgc tcgaagctgt agagacggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaanaacagc atattgacac ctggaaagac aggagatc 418

<210> 35
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 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate MSI-7

<400> 35
 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggc gactgggtta 60
 tcaaagccaa tccggctggg tgcaaagccc ctcatccga ctcgaggagg tccctggcac 120
 gtaggctgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
 gctgtctgta catgcccac gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
 ttggcaaggc ccaaaccgc tcaaagctgt agagacggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 36
 <211> 405
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate Kern217

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 ccaaccggc tgggtgcaaa gccctcatt ccgactcggg agggtcctg gcacgtaggc 120
 tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
 tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
 ggagtgcgtg accatggcgt aaggactaga ggttagagga gacccgctg taacttggca 300
 aggcccaaac ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc 360
 cttgccgtta acgcaaaaa cagcatattg acacctggaa agaca 405

<210> 37
 <211> 375
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate CoaV608

<400> 37
 cccagggcgac tgggttatca aagccaatcc ggctgggtgc aaagcccctc attccgactc 60
 gggaggggtcc ctggcacgta ggctggagag gacgcacaag tcagaccaga aatgccacct 120
 gaaagcatgc taaagggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
 acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agagggttaga 240
 ggagaccccg ctgtaacttg gcaaggccca aaccgcgtca aagctgtaga gacgggggaa 300
 ggactagagg ttagaggaga ccccttgccg ttaacgcaaa caacagcata ttgacacctg 360
 gaaagacagg agatc 375

<210> 38
 <211> 411
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate TBH-28

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 ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccagggt gactgggtta 60
 tcaaagccaa cccggctggg tgcaaagccc ctcatccga ctcgaggagg tccctggcac 120
 gtaggccgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaagggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aacctggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaat 300
 ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac a 411

<210> 39
 <211> 402
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate VR1265

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 ccggaagtca ggtaaaccgt gctgtctgta acctggcccc aggtgactgg gttatcaaag 60
 ccaatctggc tgggtgcaaa gcccctcatt ccgactcggg agggtccttg gcacgtaggc 120
 tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
 tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
 ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300
 aggcccaaac ccgctcgaag ctgtagagac gggggaagga ctagaggta gaggagacc 360
 cttgccgtca acgcaacaa cagcatattg acacctggaa ag 402

<210> 40
 <211> 374
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> 3' untranslated region of the genome of St. Louis
 encephalitis virus (SLEV) isolate CoaV353

<400> 40
 cccaggtgac tgggttatca aagccaatct agctgagtgc aaagcccctc attccgactc 60
 gggaggggtcc ctggcacgta ggctggagag gacgcaaaag tcagaccaga aatgccacct 120
 gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
 acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agagggttaga 240
 ggagaccccc ctgcaacttg gcaaggccca aaccgcctcg aagctgtaga gacgggggaa 300
 ggactagagg ttagaggaga ccccttgccg ttaacgcaa caacagcata ttgacacctg 360
 gaaagacagg agat 374

<210> 41
 <211> 27
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<220>
 <223> Dengue virus consensus upstream primer

<400> 41
 gagccccgtc caaggacgta aaaagaa 27

<210> 42
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 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

<400> 42
 gagccccgtc caaggacgta aaaagan 27

<210> 43
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dengue virus consensus upstream primer

<220>
 <221> modified_base
 <222> (26)...(26)
 <223> n = methyl-dA

<220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

<400> 43
 gagccccgtc caaggacgta aaaagnn 27

<210> 44
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dengue virus type I upstream primer

 <400> 44
 gagccccgtc caaggacgta aaatgaa 27

 <210> 45
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus type I upstream primer

 <220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

 <400> 45
 gagccccgtc caaggacgta aaatgan 27

 <210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus type I upstream primer

 <220>
 <221> modified_base
 <222> (26)...(26)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

 <400> 46
 gagccccgtc caaggacgta aaatggn 27

 <210> 47
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus types II and III upstream primer

 <400> 47
 gagccccgtc caaggacgtt aaaagaa 27

 <210> 48
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus types II and III upstream primer

<220>
 <221> misc_feature
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

 <400> 48
 gagccccgtc caaggacggtt aaaagan 27

 <210> 49
 <211> 27
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 <213> Artificial Sequence

 <220>
 <223> Dengue virus types II and III upstream primer

 <220>
 <221> modified_base
 <222> (26)...(26)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = t-butyl-benzyl-dA

 <400> 49
 gagccccgtc caaggacggtt aaaagnn 27

 <210> 50
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus type IV upstream primer

 <400> 50
 attgaagtca ggccacttgt gcca 24

 <210> 51
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus type IV upstream primer

 <220>
 <221> modified_base
 <222> (24)...(24)
 <223> n = t-butyl-benzyl-dA

 <400> 51
 attgaagtca ggccacttgt gccn 24

 <210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Dengue virus type IV upstream primer

 <220>
 <221> modified_base
 <222> (23)...(23)
 <223> n = ethyl-dC

 <220>
 <221> modified_base
 <222> (24)...(24)
 <223> n = t-butyl-benzyl-dA

 <400> 52
 attgaagtca ggccacttgt gcnn 24

 <210> 53
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus downstream primer

 <400> 53
 gatctctggt ctttcccagc gtcaa 25

 <210> 54
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus downstream primer

 <220>
 <221> modified_base
 <222> (25)...(25)
 <223> n = t-butyl-benzyl-dA

 <400> 54
 gatctctggt ctttcccagc gtcaa 25

 <210> 55
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Dengue virus downstream primer

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 <222> (24)...(24)
 <223> n = methyl-dA

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 <221> modified_base
 <222> (25)...(25)
 <223> n = t-butyl-benzyl-dA

<400> 55
 gatctctggt ctttcccagc gtcnn 25

 <210> 56
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus upstream primer

 <400> 56
 aaccgggata aaaactacgg gtggagaa 28

 <210> 57
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus upstream primer

 <220>
 <221> modified_base
 <222> (28)...(28)
 <223> n = t-butyl-benzyl-dA

 <400> 57
 aaccgggata aaaactacgg gtggagan 28

 <210> 58
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus upstream primer

 <220>
 <221> modified_base
 <222> (27)...(27)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (28)...(28)
 <223> n = t-butyl-benzyl-dA

 <400> 58
 aaccgggata aaaactacgg gtggagnn 28

 <210> 59
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus upstream primer

 <400> 59
 ataaaaacta cgggtggaga accgga 26

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus upstream primer

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 <221> modified_base
 <222> (26)...(26)
 <223> n = t-butyl-benzyl-dA

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 ataaaaacta cgggtggaga accggn 26

 <210> 61
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus downstream primer

 <400> 61
 actccggtct ttccctggcg tcaa 24

 <210> 62
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus downstream primer

 <220>
 <221> modified_base
 <222> (24)...(24)
 <223> n = t-butyl-benzyl-dA

 <400> 62
 actccggtct ttccctggcg tcan 24

 <210> 63
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> yellow fever virus downstream primer

 <220>
 <221> modified_base
 <222> (23)...(23)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (24)...(24)
 <223> n = t-butyl-benzyl-dA

<400> 63
 actccggtct ttccctggcg tcnn 24

 <210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> St Louis encephalitis virus upstream primer

 <400> 64
 caaagcccct cattccgact cggga 25

 <210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> St Louis encephalitis virus upstream primer

 <220>
 <221> modified_base
 <222> (25)...(25)
 <223> n = t-butyl-benzyl-dA

 <400> 65
 caaagcccct cattccgact cgggn 25

 <210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> St Louis encephalitis virus downstream primer

 <400> 66
 tctcctgtct ttccaggtgt caa 23

 <210> 67
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> St Louis encephalitis virus downstream primer

 <220>
 <221> modified_base
 <222> (23)...(23)
 <223> n = t-butyl-benzyl-dA

 <400> 67
 tctcctgtct ttccaggtgt can 23

 <210> 68
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> St. Louis encephalitis virus (SLEV) first primer complement
 <400> 68
 ttgacacctg gaaagacagg aga 23
 <210> 69
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> St. Louis encephalitis virus (SLEV) second primer
 <400> 69
 caaagcccct cattccgact cggg 24
 <210> 70
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> flavivirus anti-sense probe
 <400> 70
 ggggtctcctc taacctctag tccttcccc 30
 <210> 71
 <211> 98
 <212> DNA
 <213> West Nile virus
 <220>
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region
 <400> 71
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98
 <210> 72
 <211> 105
 <212> DNA
 <213> West Nile virus
 <220>
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region
 <400> 72
 tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105
 <210> 73
 <211> 121
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196835 region of conserved sequence in 3' untranslated region

<400> 73
 cagggcgaaa ggactagagg ttagaggaga cccgcggtt taaagtgcac ggcccagcct 60
 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccacaaaac 120
 a 121

<210> 74
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Example Primer 2, Japanese encephalitis virus serogroup amplification primer

<400> 74
 tctcctagtc tatcccaggt gtcaa 25

<210> 75
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> detectably-labeled oligonucleotide

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = g attached to 3' of deoxyribose phosphate backbone modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by Cy5 quencher (F)

<400> 75
 ngttagagga gaccctccag 20

<210> 76
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fluorescent moiety-quencher moiety pair in probe variant of SEQ ID NO:28

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = g attached to 3' of deoxyribose phosphate backbone modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of oligonucleotide 5'GGACTAGA3', where 5' G is modified by Cy5 quencher (F)

<220>
 <221> modified_base
 <222> (20)...(20)
 <223> n = phosphorylated g

<400> 76
 ngtttagagga gacccccgcgn 20

<210> 77
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fluorescent moiety-quencher moiety pair in probe
 variant of SEQ ID NO:28

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = g attached to 3' of deoxyribose phosphate backbone
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
 of oligonucleotide 5'GGA-5-methyl-dC-propynyl-dU-AGA3',
 where 5' G is modified by Cy5 quencher (F)

<220>
 <221> modified_base
 <222> (3)...(4)
 <223> n = propynyl-dU

<220>
 <221> modified_base
 <222> (13)...(18)
 <223> n = 5-methyl-dC

<220>
 <221> modified_base
 <222> (20)...(20)
 <223> n = phosphorylated g

<400> 77
 ngnnagagga gannnnngn 20

<210> 78
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fluorescent moiety-quencher moiety pair in probe
 variant of SEQ ID NO:70

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = t attached to 3' of deoxyribose phosphate backbone
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
 of oligonucleotide 5'GGGTCTCC3', where 5' G is modified by
 Cy5 quencher (F)

<220>
 <221> modified_base
 <222> (22)...(22)
 <223> n = phosphorylated c

<400> 78
 nctaacctct agtccttccc cn 22

<210> 79
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fluorescent moiety-quencher moiety pair in probe
 variant of SEQ ID NO:70

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = propynyl-dU attached to 3' of deoxyribose phosphate backbone
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of
 oligonucleotide 5'GGG-propynyl-dU-5-methyl-dC-propynyl-dU-5-methyl-
 dC-5-methyl-dC3', where 5' G is modified by Cy5 quencher (F)

<220>
 <221> modified_base
 <222> (2)...(2)
 <223> n = 5-methyl-dC

<220>
 <221> modified_base
 <222> (3)...(3)
 <223> n = propynyl-dU

<220>
 <221> modified_base
 <222> (22)...(22)
 <223> n = phosphorylated c

<400> 79
 nnnaacctct agtccttccc cn 22

<210> 80
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fluorescent moiety-quencher moiety pair in probe
 variant of SEQ ID NO:25

<220>
 <221> modified_base
 <222> (1)...(1)
 <223> n = g attached to 3' of deoxyribose phosphate backbone
 modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
 of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by
 Cy5 quencher (F)

<220>
 <221> modified_base
 <222> (20)...(20)
 <223> n = phosphorylated g

<400> 80
 ngtttagagga gaccctccan 20

<210> 81
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260968 region of
 conserved sequence in 3' untranslated region

<400> 81
 caaccccagg aggactgggt gaacaaagct gcgagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 82
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260969 region of
 conserved sequence in 3' untranslated region

<400> 82
 caaccccagg aggactgggt gaacaaagcc gcgagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 83
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF481864 region of
 conserved sequence in 3' untranslated region

<400> 83
 caaccccagg aggactgggt gaacaaagcc gcgagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 84
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain M12294 region of
 conserved sequence in 3' untranslated region

<400> 84
 caaccccagg aggactgggt gaccaaagct gcgagtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggacccca cgtgctttag cctcaaag 98

<210> 85
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF206518 region of
 conserved sequence in 3' untranslated region

<400> 85
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 86
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF317203 region of
 conserved sequence in 3' untranslated region

<400> 86
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 87
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF202541 region of
 conserved sequence in 3' untranslated region

<400> 87
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 88
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF404757 region of
 conserved sequence in 3' untranslated region

<400> 88
 caaccccagg aggactgggt gaacaaagcc gtgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 89
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF404753 region of
 conserved sequence in 3' untranslated region

<400> 89
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 90
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404754 region of
conserved sequence in 3' untranslated region

<400> 90
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 91
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404755 region of
conserved sequence in 3' untranslated region

<400> 91
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 92
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404756 region of
conserved sequence in 3' untranslated region

<400> 92
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 93
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF017254 region of
conserved sequence in 3' untranslated region

<400> 93
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 94
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain L48977 region of
conserved sequence in 3' untranslated region

<400> 94
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag caggacccca cgtgcttttag cctcaaag 98

<210> 95
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196536 region of
 conserved sequence in 3' untranslated region

<400> 95
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 96
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196537 region of
 conserved sequence in 3' untranslated region

<400> 96
 caaccccagg aggactgggt gaacaaagct gcgagcgat ccatgtaagc cctcagaacc 60
 gtctcggaag taggacccca catgttgtag ctccaaag 98

<210> 97
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196538 region of
 conserved sequence in 3' untranslated region

<400> 97
 caaccccagg aggactgggt gaacaaagct gcgagcgat ccatgtaagc cctcagaacc 60
 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 98
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196540 region of
 conserved sequence in 3' untranslated region

<400> 98
 caaccccagg aggactgggt gaacaaagct gcgagcgat ccatgtaagc cctcagaacc 60
 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 99
 <211> 98
 <212> DNA
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF196541 region of
      conserved sequence in 3' untranslated region

<400> 99
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                               98

<210> 100
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF196542 region of
      conserved sequence in 3' untranslated region

<400> 100
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                               98

<210> 101
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF196543 region of
      conserved sequence in 3' untranslated region

<400> 101
caaccccagg aggactgggt taccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60
gtctcggaag gaggacccca cgtgttttag cctcaagg                               98

<210> 102
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF297840 region of
      conserved sequence in 3' untranslated region

<400> 102
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
gcctcggaag gaggacccca catgttgtag cttcaagg                               98

<210> 103
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458343 region of
      conserved sequence in 3' untranslated region

<400> 103
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc ccccagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaagg                               98

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<210> 104
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458344 region of
 conserved sequence in 3' untranslated region

 <400> 104
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

 <210> 105
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458347 region of
 conserved sequence in 3' untranslated region

 <400> 105
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

 <210> 106
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458348 region of
 conserved sequence in 3' untranslated region

 <400> 106
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

 <210> 107
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458350 region of
 conserved sequence in 3' untranslated region

 <400> 107
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

 <210> 108
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458352 region of
 conserved sequence in 3' untranslated region

<400> 108
 caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60
 gcctcggaag taggacccca catgttgtag ttycaaag 98

<210> 109
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458353 region of
 conserved sequence in 3' untranslated region

<400> 109
 caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60
 gtctcggaag taggacccca catgttgtag ttccaaag 98

<210> 110
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458355 region of
 conserved sequence in 3' untranslated region

<400> 110
 caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 111
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458358 region of
 conserved sequence in 3' untranslated region

<400> 111
 caaccccagg aggactgggt taccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggacccca cgtgttttag cctcaagg 98

<210> 112
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458360 region of
 conserved sequence in 3' untranslated region

<400> 112
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 113
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458361 region of
 conserved sequence in 3' untranslated region

<400> 113
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 114
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF208017 region of
 conserved sequence in 3' untranslated region

<400> 114
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

<210> 115
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196539 region of
 conserved sequence in 3' untranslated region

<400> 115
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

<210> 116
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF196535 region of
 conserved sequence in 3' untranslated region

<400> 116
 caaccccagg aggactgggt gaccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaagg 98

<210> 117
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF458359 region of
 conserved sequence in 3' untranslated region

<400> 117
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

<210> 118
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458357 region of
 conserved sequence in 3' untranslated region

 <400> 118
 caaccccagg aggactgggt gaccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

 <210> 119
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458354 region of
 conserved sequence in 3' untranslated region

 <400> 119
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

 <210> 120
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458349 region of
 conserved sequence in 3' untranslated region

 <400> 120
 caaccccagg aggactgggt gaccaaacct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

 <210> 121
 <211> 98
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458345 region of
 conserved sequence in 3' untranslated region

 <400> 121
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60
 gtctcggaag gaggaccca cgtgcttttag cctcaaag 98

 <210> 122
 <211> 99
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF458346 region of
 conserved sequence in 3' untranslated region

<400> 122
 caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc ctctcagaac 60
 cgtttcggaa ggaggacccc acgtgcttta gcccctaaag 99

<210> 123
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF533540 region of
 conserved sequence in 3' untranslated region

<400> 123
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 124
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY187012 region of
 conserved sequence in 3' untranslated region

<400> 124
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 125
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY187013 region of
 conserved sequence in 3' untranslated region

<400> 125
 caaccccagg aggactgggt gaacaaagcc gcgaggtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 126
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY187014 region of
 conserved sequence in 3' untranslated region

<400> 126
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 127
 <211> 98
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY187015 region of
 conserved sequence in 3' untranslated region

<400> 127
 caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

<210> 128
 <211> 98
 <212> DNA
 <213> West Nile virus

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 gtttcggaac gaggaccca cgtgtttag ct 92

<210> 130
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 <212> DNA
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<220>
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 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

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 <212> DNA
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 <213> Kunjin virus

 <220>
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 sequence in 3' untranslated region

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<220>
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 sequence in 3' untranslated region

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<220>
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 sequence in 3' untranslated region

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<220>
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 sequence in 3' untranslated region

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<220>
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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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<210> 151
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 sequence in 3' untranslated region

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<210> 152
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 sequence in 3' untranslated region

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<210> 153
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 sequence in 3' untranslated region

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<210> 154
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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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<210> 158
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<220>
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 sequence in 3' untranslated region

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<210> 159
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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 sequence in 3' untranslated region

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 <210> 164
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 sequence in 3' untranslated region

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<210> 165
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<220>
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 of conserved sequence in 3' untranslated region

<400> 165
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<220>
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<400> 166
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<210> 167
 <211> 99
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<210> 168
 <211> 99
 <212> DNA
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<210> 169
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<220>
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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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<220>
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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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<220>
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 of conserved sequence in 3' untranslated region

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<220>
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 of conserved sequence in 3' untranslated region

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<220>
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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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 <212> DNA
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<220>
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 of conserved sequence in 3' untranslated region

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 of conserved sequence in 3' untranslated region

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<220>
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<220>
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<210> 197
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<220>
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<400> 197
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<210> 198
 <211> 99
 <212> DNA
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<220>
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 of conserved sequence in 3' untranslated region

<400> 198
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 199
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 199
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 200
 <211> 99
 <212> DNA
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<220>
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 of conserved sequence in 3' untranslated region

<400> 200
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 cgtctcggaa gtaggtccct gtcaccgga agttgaaag 99

<210> 201
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 201
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 cgtctcggaa gtaggtccct gtcaccgga agttgaaag 99

<210> 202
 <211> 99
 <212> DNA
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 <220>
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 of conserved sequence in 3' untranslated region

 <400> 202
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 <210> 203
 <211> 99
 <212> DNA
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 <220>
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 of conserved sequence in 3' untranslated region

 <400> 203
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

 <210> 204
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
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 of conserved sequence in 3' untranslated region

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 <210> 205
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 <220>
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 of conserved sequence in 3' untranslated region

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 cgtctcggaa gtaggtccct gtcaccgga agttgaaag 99

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 <211> 99
 <212> DNA
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 <220>
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 of conserved sequence in 3' untranslated region

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<210> 207
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

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<210> 208
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 208
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 209
 <211> 99
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<220>
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 of conserved sequence in 3' untranslated region

<400> 209
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<210> 210
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<220>
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 of conserved sequence in 3' untranslated region

<400> 210
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 211
 <211> 99
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<220>
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 of conserved sequence in 3' untranslated region

<400> 211
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 212
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain L54071 region
 of conserved sequence in 3' untranslated region

<400> 212
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 213
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain L54072 region
 of conserved sequence in 3' untranslated region

<400> 213
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 214
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain L54122 region
 of conserved sequence in 3' untranslated region

<400> 214
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<210> 215
 <211> 99
 <212> DNA
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<220>
 <223> Japanese encephalitis virus strain L54123 region
 of conserved sequence in 3' untranslated region

<400> 215
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 cgtctcggaa gtaggtccct gtcaccgga agttggaag 99

<210> 216
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF306514 region
 of conserved sequence in 3' untranslated region

 <400> 216
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 cgtctcggaa gctcctccct tctcaccgga agttgaaag 99

 <210> 217
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF306515 region
 of conserved sequence in 3' untranslated region

 <400> 217
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99

 <210> 218
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF306516 region
 of conserved sequence in 3' untranslated region

 <400> 218
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99

 <210> 219
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF306517 region
 of conserved sequence in 3' untranslated region

 <400> 219
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 cgtttcggaa gtaggtccct tctcactgga agttgaaag 99

 <210> 220
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain BFS1750-C
 region of conserved sequence in 3' untranslated
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<400> 220
 tggccccagg tgactgggtt atcaaagcca atctggccga gtgcaaagcc cctcattccg 60
 actcgggagg gtccctagca cgtaggctgg agaggac 97

<210> 221
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain 1750-Std
 region of conserved sequence in 3' untranslated
 region

<400> 221
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 actcgggagg gtccctagca cgtaggctgg agaggac 97

<210> 222
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TD6-4G-C
 region of conserved sequence in 3' untranslated
 region

<400> 222
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 actcgggagg gtccctggca cgtaggctgg agaggac 97

<210> 223
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TD6-4G-20
 region of conserved sequence in 3' untranslated
 region

<400> 223
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 actcgggagg gtccctggca cgtaggctgg agaggac 97

<210> 224
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV750
 region of conserved sequence in 3' untranslated
 region

<400> 224
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 attcgggagg gtccctggca cgtaggctgg agaggac 97

<210> 225
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain L695121.05
 region of conserved sequence in 3' untranslated
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 <400> 225
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 actcgggagg gtccctggca ttaggctgg agaggac 97

 <210> 226
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain TNM771K-C
 region of conserved sequence in 3' untranslated
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 <400> 226
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 actcgggagg gtccctggca ctaggctgg agaggac 97

 <210> 227
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain MSI-7-C
 region of conserved sequence in 3' untranslated
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 <400> 227
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 actcgggagg gtccctggca ctaggctgg agaggac 97

 <210> 228
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain Kern217
 region of conserved sequence in 3' untranslated
 region

 <400> 228
 tggccccagg cgactgggtt atcaaagcca acccggctgg gtgcaaagcc cctcattccg 60
 actcgggagg gtccctggca ctaggctgg agaggac 97

 <210> 229
 <211> 93
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV608
 region of conserved sequence in 3' untranslated
 region

<400> 229
 cccagggcgac tgggttatca aagccaatcc ggctgggtgc aaagcccctc attccgactc 60
 gggaggggtcc ctggcacgta ggctggagag gac 93

<210> 230
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TBH-28
 region of conserved sequence in 3' untranslated
 region

<400> 230
 tggccccagg tgactgggtt atcaaagcca acccggctgg gtgcaaagcc cctcattccg 60
 actcgggagg gtccctggca cgtaggcccg agaggac 97

<210> 231
 <211> 97
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain VR1265
 region of conserved sequence in 3' untranslated
 region

<400> 231
 tggccccagg tgactgggtt atcaaagcca atctggctgg gtgcaaagcc cctcattccg 60
 actcgggagg gtccctggca cgtaggctgg agcggac 97

<210> 232
 <211> 93
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV353
 region of conserved sequence in 3' untranslated
 region

<400> 232
 cccaggtgac tgggttatca aagccaatct agctgagtgc aaagcccctc attccgactc 60
 gggaggggtcc ctggcacgta ggctggagag gac 93

<210> 233
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain VR77
 region of conserved sequence in 3' untranslated
 region

<400> 233
 caaccccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 234
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain AF161266
 region of conserved sequence in 3' untranslated
 region

<400> 234
 caaccccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 235
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain M35172
 region of conserved sequence in 3' untranslated
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<400> 235
 caaccccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 236
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain L48972
 region of conserved sequence in 3' untranslated
 region

<400> 236
 caaccccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc ctccaacaa tggagatgaa 100

<210> 237
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain L48973
 region of conserved sequence in 3' untranslated
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<400> 237
 caaccccagg aggactgggt taccaaagct gattttccac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc ctgccaacaa tggagatgaa 100

<210> 238
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

 <220>
 <223> Murray Valley encephalitis virus strain L48974
 region of conserved sequence in 3' untranslated
 region

 <400> 238
 caacccagg aggactgggt taccaaagct gactctctac gggtggaaag cctcccagac 60
 ccgtctcgga agaggagccc ctgccaacaa tggagatgaa 100

 <210> 239
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

 <220>
 <223> Murray Valley encephalitis virus strain L48975
 region of conserved sequence in 3' untranslated
 region

 <400> 239
 caacccagg aggactgggt taccaaaact gactctctac gggtggaaag cctcccagaa 60
 ccgtctcgga agaggagtcc cttccaacaa tggagatgaa 100

 <210> 240
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

 <220>
 <223> Murray Valley encephalitis virus strain L48976
 region of conserved sequence in 3' untranslated
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 <400> 240
 caacccagg aggactgggt taccaaagct gattctccac gggtggaaag cctcccagaa 60
 ccgtttcgga agaggagtcc ctgctaacaa tggagatgaa 100

 <210> 241
 <211> 98
 <212> DNA
 <213> Koutango virus

 <220>
 <223> Koutango virus strain L48980 region of conserved
 sequence in 3' untranslated region

 <400> 241
 caacccagg aggactgggt caacaaatct gcgaggagat ccacgtaatc cctcagaacc 60
 gtctcggaag gaggacccca cgtgttttat tctcaaag 98

 <210> 242
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260967 region of
 conserved sequence in 3' untranslated region

<400> 242
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 243
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260968 region of
 conserved sequence in 3' untranslated region

<400> 243
 tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 244
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260969 region of
 conserved sequence in 3' untranslated region

<400> 244
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 245
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF481864 region of
 conserved sequence in 3' untranslated region

<400> 245
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 246
 <211> 103
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain M12294 region of
 conserved sequence in 3' untranslated region

<400> 246
 tggctgaagc tgtaagccaa gggaaggact agaggttaga ggagaccccg tgccaaaaaac 60
 accaaaaagaa acagcatatt gacacctggg atagactagg gga 103

<210> 247
 <211> 105
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF206518 region of
 conserved sequence in 3' untranslated region

 <400> 247
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

 <210> 248
 <211> 105
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF317203 region of
 conserved sequence in 3' untranslated region

 <400> 248
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

 <210> 249
 <211> 105
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF202541 region of
 conserved sequence in 3' untranslated region

 <400> 249
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

 <210> 250
 <211> 105
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF404757 region of
 conserved sequence in 3' untranslated region

 <400> 250
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

 <210> 251
 <211> 105
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF404753 region of
 conserved sequence in 3' untranslated region

<400> 251
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 252
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF404754 region of
 conserved sequence in 3' untranslated region

<400> 252
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 253
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF404755 region of
 conserved sequence in 3' untranslated region

<400> 253
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 254
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF404756 region of
 conserved sequence in 3' untranslated region

<400> 254
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 255
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF017254 region of
 conserved sequence in 3' untranslated region

<400> 255
 tgactgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgataacctg ggatagacta ggaga 105

<210> 256
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF533540 region of
 conserved sequence in 3' untranslated region

<400> 256
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 257
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY262283 region of
 conserved sequence in 3' untranslated region

<400> 257
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 258
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY278441 region of
 conserved sequence in 3' untranslated region

<400> 258
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 259
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY268132 region of
 conserved sequence in 3' untranslated region

<400> 259
 tggctgaagc tgtagggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 260
 <211> 105
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY268133 region of
 conserved sequence in 3' untranslated region

<400> 260
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 caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 261
 <211> 105
 <212> DNA
 <213> Kunjin virus

 <220>
 <223> Kunjin virus strain AY274504 region of conserved
 sequence in 3' untranslated region

 <400> 261
 tggctgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccgcaaaa 60
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 <210> 262
 <211> 105
 <212> DNA
 <213> Kunjin virus

 <220>
 <223> Kunjin virus strain AY274505 region of conserved
 sequence in 3' untranslated region

 <400> 262
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 caccacaaca acacagcata ttgacacctg ggatagacta ggaga 105

 <210> 263
 <211> 105
 <212> DNA
 <213> Kunjin virus

 <220>
 <223> Kunjin virus strain L24512 region of conserved
 sequence in 3' untranslated region

 <400> 263
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 caccacaaca acacagcata ttgacacctg ggatagacta ggaga 105

 <210> 264
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AB051292 region
 of conserved sequence in 3' untranslated region

 <400> 264
 cccctcgaag ctgtggagga ggtggaagga ctagaggta gaggagacc cgcatttgca 60
 tcaaaacagc atattgacac ctgggaatag actgggaga 99

 <210> 265
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF014160 region
 of conserved sequence in 3' untranslated region

<400> 265
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 266
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF014161 region
 of conserved sequence in 3' untranslated region

<400> 266
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 267
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF045551 region
 of conserved sequence in 3' untranslated region

<400> 267
 cccctcgaag ctgtagagga ggtgtaagga atagagggtta gaggagaccc cgcaatttgc 60
 atcaaacagc atattgacac ctgggaatag agtgggaga 99

<210> 268
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF069076 region
 of conserved sequence in 3' untranslated region

<400> 268
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 269
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 269
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 270
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF080251 region
 of conserved sequence in 3' untranslated region

<400> 270
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 271
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF098735 region
 of conserved sequence in 3' untranslated region

<400> 271
 ctccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 272
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF098736 region
 of conserved sequence in 3' untranslated region

<400> 272
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 273
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 273
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggataga ctgggaga 98

<210> 274
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF217620 region
 of conserved sequence in 3' untranslated region

<400> 274
 ttccctcgaag ctgtagagga agtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 275
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF221499 region
 of conserved sequence in 3' untranslated region

 <400> 275
 ctccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 276
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF221500 region
 of conserved sequence in 3' untranslated region

 <400> 276
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 277
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 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF254452 region
 of conserved sequence in 3' untranslated region

 <400> 277
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 278
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF254453 region
 of conserved sequence in 3' untranslated region

 <400> 278
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 279
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF315119 region
 of conserved sequence in 3' untranslated region

<400> 279
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 280
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF416457 region
 of conserved sequence in 3' untranslated region

<400> 280
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 281
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF486638 region
 of conserved sequence in 3' untranslated region

<400> 281
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaatata ctgggaga 98

<210> 282
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain U14163 region
 of conserved sequence in 3' untranslated region

<400> 282
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 283
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain U15763 region
 of conserved sequence in 3' untranslated region

<400> 283
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 284
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain L48961 region
 of conserved sequence in 3' untranslated region

<400> 284
 ctccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 285
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain U47032 region
 of conserved sequence in 3' untranslated region

<400> 285
 cccctcgaag ctgtagagga ggtggagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctaggaga 98

<210> 286
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 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain M18370 region
 of conserved sequence in 3' untranslated region

<400> 286
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 287
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain M55506 region
 of conserved sequence in 3' untranslated region

<400> 287
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 288
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 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 288
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 289
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain D90195 region
 of conserved sequence in 3' untranslated region

 <400> 289
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 290
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 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain D90194 region
 of conserved sequence in 3' untranslated region

 <400> 290
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 291
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF311748 region
 of conserved sequence in 3' untranslated region

 <400> 291
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 tcaaacagca tattgacacc tgggaataga ctgggaga 98

 <210> 292
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AY184212 region
 of conserved sequence in 3' untranslated region

 <400> 292
 cccttcgaag ctgtagaaga ggtggaagga ctagagggtta gaggagaccc cgcattctgca 60
 tcaaacagca tattgacacc tgggaataga ctaggaga 98

 <210> 293
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AY316157 region
 of conserved sequence in 3' untranslated region

<400> 293
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcaatttgc 60
 atcaaacagc atattgacac ctgggaatag actgggaga 99

<210> 294
 <211> 99
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306514 region
 of conserved sequence in 3' untranslated region

<400> 294
 cccctcgaag ctgtagagga ggtgtaagga atagagggtta gaggagaccc cgcaatttgc 60
 atcaaacagc atattgacac ctgggaatag agtgggaga 99

<210> 295
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306515 region
 of conserved sequence in 3' untranslated region

<400> 295
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 296
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306516 region
 of conserved sequence in 3' untranslated region

<400> 296
 cccctcgaag ctgtagaggg ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 297
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306517 region
 of conserved sequence in 3' untranslated region

<400> 297
 cccctcgaag ctgtagagga ggtggaagga ctagagggtta gaggagaccc cgcatttgca 60
 tcaaacagca tattgacacc tgggaataga gtgggaga 98

<210> 298
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain D00037 region
 of conserved sequence in 3' untranslated region

<400> 298
 cctctttagtag cttttgaggt ggttgaaggt cttgaggttt gaggagtccc cgtctttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 299
 <211> 98
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain M14933 region
 of conserved sequence in 3' untranslated region

<400> 299
 cctctttagtag cttttgaggt ggttgaaggt cttgaggttt gaggagtccc cgtctttgca 60
 tcaaacagca tattgacacc tgggaataga ctgggaga 98

<210> 300
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 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain BFS1750-C
 region of conserved sequence in 3' untranslated
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<400> 300
 ccgctcgaag ctgtagagac gggggaagga ctagaggta gaggagaccc cttgccgtta 60
 acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 301
 <211> 27
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain 1750-Std
 region of conserved sequence in 3' untranslated
 region

<400> 301
 ccgctcgaag ctgtagagac gggggaa 27

<210> 302
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TD6-4G-C
 region of conserved sequence in 3' untranslated
 region

<400> 302
 ccgctcgaag ctgtagagat gggggaagga ctagaggta gaggagaccc cttgccgtta 60
 acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 303
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain TD6-4G-20
 region of conserved sequence in 3' untranslated
 region

 <400> 303
 ccgctcgaag ctgtagagat gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacia cagcatattg acacctggaa agacaggaga 100

 <210> 304
 <211> 27
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain CoaV750
 region of conserved sequence in 3' untranslated
 region

 <400> 304
 ccgctcgaag ctgtagagat gggggaa 27

 <210> 305
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain L695121.05
 region of conserved sequence in 3' untranslated
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 <400> 305
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacia cagcatattg acacctggaa agacaggaga 100

 <210> 306
 <211> 100
 <212> DNA
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 <220>
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 region of conserved sequence in 3' untranslated
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<210> 307
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain MSI-7-C
 region of conserved sequence in 3' untranslated
 region

<400> 307
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 308
 <211> 95
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain Kern217
 region of conserved sequence in 3' untranslated
 region

<400> 308
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 309
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV608
 region of conserved sequence in 3' untranslated
 region

<400> 309
 ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 310
 <211> 95
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TBH-28
 region of conserved sequence in 3' untranslated
 region

<400> 310
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 311
 <211> 92
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain VR1265
 region of conserved sequence in 3' untranslated
 region

<400> 311
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtca 60
 acgcaaaca cagcatattg acacctggaa ag 92

<210> 312
 <211> 100
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV353
 region of conserved sequence in 3' untranslated
 region

<400> 312
 ccgctcgaag ctgtagagac gggggaagga ctagagggtta gaggagaccc cttgccgtta 60
 acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 313
 <211> 104
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain VR77
 region of conserved sequence in 3' untranslated
 region

<400> 313
 tcgccgaagc tgtaaggcgg gtggacggac tagagggttag aggagacccc actctcaaaa 60
 gcatcaaaca acagcatatt gacacctggg aaaagactag gaga 104

<210> 314
 <211> 104
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain AF161266
 region of conserved sequence in 3' untranslated
 region

<400> 314
 tcgccgaagc tgtaaggcgg gtggacggac tagagggttag aggagacccc actctcaaaa 60
 gcatcaaaca acagcatatt gacacctggg aaaagactag gaga 104

<210> 315
 <211> 100
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain M35172
 region of conserved sequence in 3' untranslated
 region

<400> 315
 tcgccgaagc tgtaaggcgg gtggacggac tagaggtttag aggagacccc actctcaaaa 60
 gcatcaaaaca acagcatatt gacacctggg aaaagactag 100

<210> 316
 <211> 121
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260967 region of
 conserved sequence in 3' untranslated region

<400> 316
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
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 a 121

<210> 317
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 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260968 region of
 conserved sequence in 3' untranslated region

<400> 317
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 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
 a 121

<210> 318
 <211> 121
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF260969 region of
 conserved sequence in 3' untranslated region

<400> 318
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 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
 a 121

<210> 319
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 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF481864 region of
 conserved sequence in 3' untranslated region

<400> 319
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 gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
 a 121

<210> 320
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 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain M12294 region of
 conserved sequence in 3' untranslated region

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 <210> 321
 <211> 121
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF206518 region of
 conserved sequence in 3' untranslated region

 <400> 321
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 a 121

 <210> 322
 <211> 121
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF317203 region of
 conserved sequence in 3' untranslated region

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 a 121

 <210> 323
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 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AF202541 region of
 conserved sequence in 3' untranslated region

 <400> 323
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 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
 a 121

 <210> 324
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 <212> DNA
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF404757 region of
      conserved sequence in 3' untranslated region

<400> 324
cagggcgaaa ggactagagg ttagaggaga cccgcggtt tgaagagcac ggcccagcct 60
ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 325
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404753 region of
      conserved sequence in 3' untranslated region

<400> 325
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ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 326
<211> 121
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404754 region of
      conserved sequence in 3' untranslated region

<400> 326
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ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 327
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<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404755 region of
      conserved sequence in 3' untranslated region

<400> 327
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ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a                                                    121

<210> 328
<211> 121
<212> DNA
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<220>
<223> West Nile virus strain AF404756 region of
      conserved sequence in 3' untranslated region

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 a 121

<210> 329
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 <212> DNA
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<220>
 <223> West Nile virus strain AF017254 region of
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<400> 329
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
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 a 121

<210> 330
 <211> 87
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF208017 region of
 conserved sequence in 3' untranslated region

<400> 330
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 ggctgaagct gtaagccaag ggaagga 87

<210> 331
 <211> 121
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AF533540 region of
 conserved sequence in 3' untranslated region

<400> 331
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<210> 332
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 <212> DNA
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<220>
 <223> West Nile virus strain AY262283 region of
 conserved sequence in 3' untranslated region

<400> 332
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 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccgcaaaaac 120
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<210> 333
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 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AY277251 region of
 conserved sequence in 3' untranslated region

 <400> 333
 caaggagaag ggactagagg ttagcggaga ccctgcgcat atagaaagag aggcacggcc 60
 cagcctgaca gaagctgtaa gtcaggggaa ggact 95

 <210> 334
 <211> 118
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AY277252 region of
 conserved sequence in 3' untranslated region

 <400> 334
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccatggc 60
 tgaagctgta ggtcagggga aggactagag gttagtggag accccgtgcc aaaaaaca 118

 <210> 335
 <211> 59
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AY278441 region of
 conserved sequence in 3' untranslated region

 <400> 335
 cagggcgaaa ggactagagg ttagaggaga ccccgcggtt tgaagtgcac ggcccagcc 59

 <210> 336
 <211> 115
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AY278442 region of
 conserved sequence in 3' untranslated region

 <400> 336
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 <210> 337
 <211> 121
 <212> DNA
 <213> West Nile virus

 <220>
 <223> West Nile virus strain AY268132 region of
 conserved sequence in 3' untranslated region

<400> 337
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 ggctgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccacaaaac 120
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<210> 338
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 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY268133 region of conserved sequence in 3' untranslated region

<400> 338
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<210> 339
 <211> 59
 <212> DNA
 <213> West Nile virus

<220>
 <223> West Nile virus strain AY490240 region of conserved sequence in 3' untranslated region

<400> 339
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<210> 340
 <211> 121
 <212> DNA
 <213> Kunjin virus

<220>
 <223> Kunjin virus strain AY274504 region of conserved sequence in 3' untranslated region

<400> 340
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<210> 341
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 <212> DNA
 <213> Kunjin virus

<220>
 <223> Kunjin virus strain AY274505 region of conserved sequence in 3' untranslated region

<400> 341
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 a 121

<210> 342
 <211> 121
 <212> DNA
 <213> Kunjin virus

 <220>
 <223> Kunjin virus strain L24512 region of conserved
 sequence in 3' untranslated region

 <400> 342
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 <210> 343
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 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AB051292 region
 of conserved sequence in 3' untranslated region

 <400> 343
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 atcaa 125

 <210> 344
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF014160 region
 of conserved sequence in 3' untranslated region

 <400> 344
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 atcaa 125

 <210> 345
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF014161 region
 of conserved sequence in 3' untranslated region

 <400> 345
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 atcaa 125

 <210> 346
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF045551 region
 of conserved sequence in 3' untranslated region

<400> 346
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 cccctcgaa gctgtagagg aggtgtaagg aatagagggt agaggagacc ccgcaatttg 120
 catca 125

<210> 347
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF069076 region
 of conserved sequence in 3' untranslated region

<400> 347
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 348
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF075723 region
 of conserved sequence in 3' untranslated region

<400> 348
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa ataacaacat gcggcccaag 60
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 atcaa 125

<210> 349
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF080251 region
 of conserved sequence in 3' untranslated region

<400> 349
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 350
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF098735 region
 of conserved sequence in 3' untranslated region

<400> 350
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 351
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF098736 region
 of conserved sequence in 3' untranslated region

<400> 351
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 atcaa 125

<210> 352
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF098737 region
 of conserved sequence in 3' untranslated region

<400> 352
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 atcaa 125

<210> 353
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF217620 region
 of conserved sequence in 3' untranslated region

<400> 353
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 atcaa 125

<210> 354
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 354
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaataacat gcggcccaag 60
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 atcaa 125

<210> 355
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
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 of conserved sequence in 3' untranslated region

 <400> 355
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 atcaa 125

 <210> 356
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
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 of conserved sequence in 3' untranslated region

 <400> 356
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 atcaa 125

 <210> 357
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
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 of conserved sequence in 3' untranslated region

 <400> 357
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 atcaa 125

 <210> 358
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

 <220>
 <223> Japanese encephalitis virus strain AF315119 region
 of conserved sequence in 3' untranslated region

 <400> 358
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 atcaa 125

 <210> 359
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF416457 region
 of conserved sequence in 3' untranslated region

<400> 359
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60
 cccctcgaa gctgtagagg aggtggaagg actagagggtt agaggagacc ccgcatttgc 120
 atcaa 125

<210> 360
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF486638 region
 of conserved sequence in 3' untranslated region

<400> 360
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 atcaa 125

<210> 361
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain U14163 region
 of conserved sequence in 3' untranslated region

<400> 361
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 atcaa 125

<210> 362
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain U15763 region
 of conserved sequence in 3' untranslated region

<400> 362
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 atcaa 125

<210> 363
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain L48961 region
 of conserved sequence in 3' untranslated region

<400> 363
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 atcaa 125

<210> 364
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 364
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 365
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain M18370 region
 of conserved sequence in 3' untranslated region

<400> 365
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaatat gcggcccaag 60
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 atcaa 125

<210> 366
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain M55506 region
 of conserved sequence in 3' untranslated region

<400> 366
 cgaggtgtaa ggactagagg ttagaggaga ccccggtggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 367
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 367
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 atcaa 125

<210> 368
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain D90195 region
 of conserved sequence in 3' untranslated region

<400> 368
 cgaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaatat gcggcccaag 60
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 atcaa 125

<210> 369
 <211> 125
 <212> DNA
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<220>
 <223> Japanese encephalitis virus strain D90194 region
 of conserved sequence in 3' untranslated region

<400> 369
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 atcaa 125

<210> 370
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
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 of conserved sequence in 3' untranslated region

<400> 370
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 atcaa 125

<210> 371
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AY184212 region
 of conserved sequence in 3' untranslated region

<400> 371
 cgagatgtaa ggactagagg ttagaggaga ccccgtaggaa acaacaacat gcggcccaag 60
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 atcaa 125

<210> 372
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AY316157 region
 of conserved sequence in 3' untranslated region

<400> 372
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 catca 125

<210> 373
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306514 region
 of conserved sequence in 3' untranslated region

<400> 373
 ttaggtgtaa ggactagagg ttagaggaga ccccgtaggaa acaaaattat gcggcccaag 60
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 catca 125

<210> 374
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306515 region
 of conserved sequence in 3' untranslated region

<400> 374
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 atcaa 125

<210> 375
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306516 region
 of conserved sequence in 3' untranslated region

<400> 375
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 atcaa 125

<210> 376
 <211> 125
 <212> DNA
 <213> Japanese encephalitis virus

<220>
 <223> Japanese encephalitis virus strain AF306517 region
 of conserved sequence in 3' untranslated region

<400> 376
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 atcaa 125

<210> 377
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain BFS1750 region
 of conserved sequence in 3' untranslated region

<400> 377
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 gc 122

<210> 378
 <211> 85
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain 1750-Std region
 of conserved sequence in 3' untranslated region

<400> 378
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 gctcgaagct gtagagacgg gggaa 85

<210> 379
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TD6-4G region
 of conserved sequence in 3' untranslated region

<400> 379
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 gc 122

<210> 380
 <211> 85
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV750 region
 of conserved sequence in 3' untranslated region

<400> 380
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<210> 381
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 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain L695121.05 region
 of conserved sequence in 3' untranslated region

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 gc 122

 <210> 382
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 <212> DNA
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 <220>
 <223> St. Louis encephalitis virus strain TNM771K region
 of conserved sequence in 3' untranslated region

 <400> 382
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 gc 122

 <210> 383
 <211> 122
 <212> DNA
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 <220>
 <223> St. Louis encephalitis virus strain MSI-7 region
 of conserved sequence in 3' untranslated region

 <400> 383
 catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60
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 gc 122

 <210> 384
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

 <220>
 <223> St. Louis encephalitis virus strain Kern217 region
 of conserved sequence in 3' untranslated region

 <400> 384
 catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60
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 gc 122

 <210> 385
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV608 region
 of conserved sequence in 3' untranslated region

<400> 385
 catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60
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 gc 122

<210> 386
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain TBH-28 region
 of conserved sequence in 3' untranslated region

<400> 386
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 gc 122

<210> 387
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain VR1265 region
 of conserved sequence in 3' untranslated region

<400> 387
 catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60
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 gc 122

<210> 388
 <211> 122
 <212> DNA
 <213> St. Louis encephalitis virus

<220>
 <223> St. Louis encephalitis virus strain CoaV353 region
 of conserved sequence in 3' untranslated region

<400> 388
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 gc 122

<210> 389
 <211> 119
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain VR77
 region of conserved sequence in 3' untranslated
 region

<400> 389
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<210> 390
 <211> 119
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain AF161266
 region of conserved sequence in 3' untranslated
 region

<400> 390
 cccggcgaag gactagaggt tagaggagac cctgcggaag aaatgagtgg cccaagctcg 60
 ccgaagctgt aaggcgggtg gacggactag aggttagagg agaccccact ctcaaaagc 119

<210> 391
 <211> 119
 <212> DNA
 <213> Murray Valley encephalitis virus

<220>
 <223> Murray Valley encephalitis virus strain M35172
 region of conserved sequence in 3' untranslated
 region

<400> 391
 cccggcgaag gactagaggt tagaggagac cctgcggaag aaatgagtgg cccaagctcg 60
 ccgaagctgt aaggcgggtg gacggactag aggttagagg agaccccact ctcaaaagc 119

<210> 392
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain U88537 region of
 conserved sequence in 3' untranslated region

<400> 392
 atggggtagc agactagtgg ttagaggaga cccctcccaa gacacaacgc agcagcgggg 60
 cccaacacca ggggaagctg taccctggtg gtaaggacta gaggttagag gagaccccc 120
 gcacaacaac a 131

<210> 393
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain U88536 region of
 conserved sequence in 3' untranslated region

<400> 393
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 gcacaacaac a 131

<210> 394
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain U88535 region of
 conserved sequence in 3' untranslated region

 <400> 394
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 gcacaacaac a 131

 <210> 395
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 <212> DNA
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 <220>
 <223> Dengue virus type 1 strain M87512 region of
 conserved sequence in 3' untranslated region

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 gcataacaat a 131

 <210> 396
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 <212> DNA
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 <220>
 <223> Dengue virus type 1 strain AY206457 region of
 conserved sequence in 3' untranslated region

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 gcacaacaac a 131

 <210> 397
 <211> 101
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AY145123 region of
 conserved sequence in 3' untranslated region

 <400> 397
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 <210> 398
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 <212> DNA
 <213> Dengue virus type 1

<220>
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<400> 398
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 gcacaacaac a 131

<210> 399
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 <213> Dengue virus type 1

<220>
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<400> 399
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 gcacaacaac a 131

<210> 400
 <211> 131
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<220>
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<400> 400
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 gcacaacaac a 131

<210> 401
 <211> 131
 <212> DNA
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<220>
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<400> 401
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 gcataacaac a 131

<210> 402
 <211> 131
 <212> DNA
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<220>
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<400> 402
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 gcataacaac a 131

<210> 403
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF514878 region of
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<400> 403
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 gcacaacaac a 131

<210> 404
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF514876 region of
 conserved sequence in 3' untranslated region

<400> 404
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 cccaacacca tgggaagctg taccttgggtg gtaaggacta gaggttagag gagaccccc 120
 gcataacaac a 131

<210> 405
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF513110 region of
 conserved sequence in 3' untranslated region

<400> 405
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 cccaacacca ggggaagctg taccttgggtg gtaaggacta gaggttagag gagaccccc 120
 gcacaacaac a 131

<210> 406
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF350498 region of
 conserved sequence in 3' untranslated region

<400> 406
 atggggtagc agactagtgg ttagaggaga cccctcccaa aacacaacgc agcagcgggg 60
 cccaacacca ggggaagctg taccctgggtg gtaaggacta gaggttagag gagaccccc 120
 gcataacaat a 131

<210> 407
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AF311958 region of
 conserved sequence in 3' untranslated region

 <400> 407
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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120
 gctcaacaac a 131

 <210> 408
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AF311957 region of
 conserved sequence in 3' untranslated region

 <400> 408
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 gcacaacaac a 131

 <210> 409
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AF311956 region of
 conserved sequence in 3' untranslated region

 <400> 409
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 cccaacacca tgggaagctg taccttgggt gtaaggacta gaggttagag gagaccccc 120
 gcacaacaac a 131

 <210> 410
 <211> 97
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AF310148 region of
 conserved sequence in 3' untranslated region

 <400> 410
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 cccaacacca ggggaagctg taccctgggt gtaagga 97

 <210> 411
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF310147 region of conserved sequence in 3' untranslated region

<400> 411
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 gcataacaat a 131

<210> 412
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF310146 region of conserved sequence in 3' untranslated region

<400> 412
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 gcacaacaac a 131

<210> 413
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF309641 region of conserved sequence in 3' untranslated region

<400> 413
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 cccaacacca ggggaagctg taccctggtg gtaaggacta gaggttagag gagaccccc 120
 gcataacaat a 131

<210> 414
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
 <223> Dengue virus type 1 strain AF298808 region of conserved sequence in 3' untranslated region

<400> 414
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 gcataacaat a 131

<210> 415
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

<220>
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<400> 415
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gcacaacaac a 131

<210> 416
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF226687 region of
conserved sequence in 3' untranslated region

<400> 416
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gcacaacaac a 131

<210> 417
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF226686 region of
conserved sequence in 3' untranslated region

<400> 417
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gcacaacaac a 131

<210> 418
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF226685 region of
conserved sequence in 3' untranslated region

<400> 418
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gcacaacaac a 131

<210> 419
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF180818 region of
conserved sequence in 3' untranslated region

<400> 419
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gcgtaacaat a 131

<210> 420
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AF180817 region of
 conserved sequence in 3' untranslated region

 <400> 420
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 gcgtaacaat a 131

 <210> 421
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
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 conserved sequence in 3' untranslated region

 <400> 421
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 gcataataat a 131

 <210> 422
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain AB074760 region of
 conserved sequence in 3' untranslated region

 <400> 422
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 cccaacacca ggggaagctg taccctggtg gtaaggacta gaggttagag gagaccccc 120
 gcataacaat a 131

 <210> 423
 <211> 131
 <212> DNA
 <213> Dengue virus type 1

 <220>
 <223> Dengue virus type 1 strain VR344-3 region of
 conserved sequence in 3' untranslated region

 <400> 423
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 cccaacacca ggggaagctg taccctggtg gtaaggacta gaggttagag gagaccccc 120
 gcataacaat a 131

 <210> 424
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF022434 region of conserved sequence in 3' untranslated region

<400> 424
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca gaa 133

<210> 425
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF022435 region of conserved sequence in 3' untranslated region

<400> 425
 atggcgtagt ggactagcgg ttagaggaga cccctccctc acaaatcgca gcaacaatgg 60
 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 426
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF022436 region of conserved sequence in 3' untranslated region

<400> 426
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 427
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF022437 region of conserved sequence in 3' untranslated region

<400> 427
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 428
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF022438 region of conserved sequence in 3' untranslated region

<400> 428
atggcgtagt ggactagcgg ttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
gggcccagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 429
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022439 region of
conserved sequence in 3' untranslated region

<400> 429
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gggcccagg cgagatgaag ctgtagtctc gctggaagga atagagggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 430
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022440 region of
conserved sequence in 3' untranslated region

<400> 430
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gggcccagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 431
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022441 region of
conserved sequence in 3' untranslated region

<400> 431
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gggcccagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 432
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF038402 region of
conserved sequence in 3' untranslated region

<400> 432
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gggcccagg tgagatgaag ctgtagtctc actggaagga ctagagggtta gaggagaccc 120
ccccaaaaca aaa 133

<210> 433
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF038403 region of
 conserved sequence in 3' untranslated region

<400> 433
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaaca aaa 133

<210> 434
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100145 region of
 conserved sequence in 3' untranslated region

<400> 434
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaata aaa 133

<210> 435
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100146 region of
 conserved sequence in 3' untranslated region

<400> 435
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaagca aaa 133

<210> 436
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100147 region of
 conserved sequence in 3' untranslated region

<400> 436
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaaca aaa 133

<210> 437
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100148 region of conserved sequence in 3' untranslated region

<400> 437
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaaca aaa 133

<210> 438
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100149 region of conserved sequence in 3' untranslated region

<400> 438
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 gggcccaagg tgagatgaag ctgtagcctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaaca aaa 133

<210> 439
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100150 region of conserved sequence in 3' untranslated region

<400> 439
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaaca aaa 133

<210> 440
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100151 region of conserved sequence in 3' untranslated region

<400> 440
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 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaagaca aaa 133

<210> 441
 <211> 134
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100458 region of conserved sequence in 3' untranslated region

<400> 441
 atggcgtagt ggactagcgg ttagaggaga cccctccctt acagatcgca gcaacaatgg 60
 gggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
 ccccaaaaac aaaa 134

<210> 442
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100459 region of
 conserved sequence in 3' untranslated region

<400> 442
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 443
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
 <223> Dengue virus type 2 strain AF100460 region of
 conserved sequence in 3' untranslated region

<400> 443
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 444
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
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 conserved sequence in 3' untranslated region

<400> 444
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 445
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
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 conserved sequence in 3' untranslated region

<400> 445
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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 446
 <211> 133
 <212> DNA
 <213> Dengue virus type 2

<220>
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 conserved sequence in 3' untranslated region

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 gggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 447
 <211> 133
 <212> DNA
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<220>
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 conserved sequence in 3' untranslated region

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 gggcccaagg caagatgaag ctgtagtctc gctggaagga ctagagggtta gaggagaccc 120
 ccccgaaaca aaa 133

<210> 448
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<220>
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<400> 448
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 cccaagaca aaa 133

<210> 449
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 <212> DNA
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<220>
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 ccccaaaata aaa 133

<210> 450
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<220>
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 cccccaaaaa caaa 134

<210> 451
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<210> 452
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<210> 453
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 cccccaaaca aaa 133

<210> 454
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<220>
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<210> 455
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<212> DNA
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conserved sequence in 3' untranslated region

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<210> 456
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<212> DNA
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<220>
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conserved sequence in 3' untranslated region

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<210> 457
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conserved sequence in 3' untranslated region

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conserved sequence in 3' untranslated region

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 ccccgaaaca aaa 133

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<220>
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<210> 464
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 ccccaaaaca aaa 133

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<220>
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<210> 468
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<220>
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<210> 470
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 conserved sequence in 3' untranslated region

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 ccccaaaaca aaa 133

<210> 471
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<220>
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 cccagacaaa aaa 133

<210> 472
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 conserved sequence in 3' untranslated region

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 cccagacaaa aaaa 134

 <210> 473
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 conserved sequence in 3' untranslated region

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 cccagacaaa aaaa 134

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 cccagacaaa aaa 133

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 ggcccaaggt gtgttgaagc ttagaccaca ctggaaggac cagaggttag aggagacccc 120
 cccagacaaa aaa 133

 <210> 476
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<220>
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<210> 477
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 <212> DNA
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<220>
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<210> 478
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<220>
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<210> 479
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<220>
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<210> 481
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<220>
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 ccccgaata aaa 133

<210> 482
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<220>
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 ccccgaata aaa 133

<210> 483
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<220>
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<210> 487
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<210> 491
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<210> 492
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 <212> DNA
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<210> 494
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<210> 495
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<210> 496
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<220>
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 ccccgaaaca aaa 133

<210> 498
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<220>
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 conserved sequence in 3' untranslated region

<400> 498
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<210> 499
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 <212> DNA
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<220>
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 conserved sequence in 3' untranslated region

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 ccccgaaaca aaa 133

<210> 500
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<220>
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 ccccgaaaca aaa 133

<210> 501
 <211> 130
 <212> DNA
 <213> Dengue virus type 3

<220>
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 conserved sequence in 3' untranslated region

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 cgcaaataaa 130

<210> 502
 <211> 130
 <212> DNA
 <213> Dengue virus type 3

<220>
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 cgcaaacaaa 130

<210> 503
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 <212> DNA
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<220>
 <223> Dengue virus type 3 strain AF317645 region of conserved sequence in 3' untranslated region

<400> 503
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<210> 504
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<220>
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<400> 504
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<210> 505
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 <212> DNA
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<220>
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<400> 505
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 cgcaaataaa 130

<210> 506
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<220>
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<400> 506
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 cgcaaataaa 130

<210> 507
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<220>
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 conserved sequence in 3' untranslated region

<400> 507
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 cgcaaataaa 130

<210> 508
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<220>
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 conserved sequence in 3' untranslated region

<400> 508
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 cgcaaataaa 130

<210> 509
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<220>
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 conserved sequence in 3' untranslated region

<400> 509
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 cgcaaataaa 130

<210> 510
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 <212> DNA
 <213> Dengue virus type 3

<220>
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 conserved sequence in 3' untranslated region

<400> 510
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 cgcaaataaa 130

<210> 511
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 <213> Dengue virus type 3

 <220>
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 conserved sequence in 3' untranslated region

 <400> 511
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 acccccccaa caaa 135

 <210> 514
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<220>
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<400> 515
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<210> 516
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 <212> DNA
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<220>
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<400> 516
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<210> 517
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<220>
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 acccccccaa cacaaa 136

<210> 518
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<220>
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 acccccccaa cacaaa 136

<210> 519
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<220>
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acccccccaa cacaaa 136

<210> 520

<211> 105

<212> DNA

<213> Dengue virus type 4

<220>

<223> Dengue virus type 4 strain AF326826 region of
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agggggccca agactagagg ttagaggaga cccccccaac acaaa 105

<210> 521

<211> 105

<212> DNA

<213> Dengue virus type 4

<220>

<223> Dengue virus type 4 strain AF326827 region of
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agggggccca agactagagg ttagaggaga cccccccaac acaaa 105

<210> 522

<211> 136

<212> DNA

<213> Dengue virus type 4

<220>

<223> Dengue virus type 4 strain AF375822 region of
conserved sequence in 3' untranslated region

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<210> 523

<211> 136

<212> DNA

<213> Dengue virus type 4

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conserved sequence in 3' untranslated region

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<210> 524

<211> 136

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<220>
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 acccccccaa cacaaa 136

<210> 525
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<220>
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<210> 526
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<220>
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<210> 527
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<220>
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<210> 528
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<220>
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<400> 528
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<210> 529
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<220>
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<400> 529
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<210> 530
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<400> 530
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<210> 532
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<210> 534
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<210> 535
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<220>
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<210> 536
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 <213> Dengue virus type 4

<220>
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<220>
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<220>
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<210> 540
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<220>
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<210> 545
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 conserved sequence in 3' untranslated region

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<210> 551
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 <212> DNA
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<220>
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<210> 552
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<220>
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<210> 553
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 <212> DNA
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<210> 554
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<220>
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<210> 555
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<210> 556
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 <212> DNA
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<220>
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<210> 557
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 <212> DNA
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<220>
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 acccccccaa cacaaa 136

<210> 558
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<220>
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 acccccccaa cacaaa 136

<210> 559
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 <212> DNA
 <213> Dengue virus type 4

<220>
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<210> 560
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 <212> DNA
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<220>
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 conserved sequence in 3' untranslated region

<400> 560
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<210> 561
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 <212> DNA
 <213> Dengue virus type 4

<220>
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<400> 561
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 agggggcccg aagccaggag gaagctgtac tcctggtgga aggactagag gtttagaggag 120
 acccccccaa cacaaa 136

<210> 562
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 <212> DNA
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<220>
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 conserved sequence in 3' untranslated region

<400> 562
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 acccccccaa cacaaa 136

<210> 563
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<220>
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<400> 563
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 agggggcccg aagccaggag gaagctgtac tcctggtgga aggactagag gttagaggag 120
 acccccccaa cacaaa 136

<210> 564
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<220>
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<210> 565
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<220>
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<400> 565
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<210> 566
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<220>
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<400> 566
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 acccccccaa cacaaa 136

<210> 567
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<220>
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<400> 567
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 acccccccaa cacaaa 136

<210> 568
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<220>
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 conserved sequence in 3' untranslated region

<400> 568
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 acccccccaa cacaaa 136

<210> 569
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<220>
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 conserved sequence in 3' untranslated region

<400> 569
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 acccccccaa cacaaa 136

<210> 570
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 conserved sequence in 3' untranslated region

<400> 570
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 acccccccaa cacaaa 136

<210> 571
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<220>
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 conserved sequence in 3' untranslated region

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<210> 572
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 acccccccaa cacaaa 136

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 conserved sequence in 3' untranslated region

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 acccccccaa cacaaa 136

 <210> 574
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 conserved sequence in 3' untranslated region

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 acccccccaa cacaaa 136

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 acccccccaa cacaaa 136

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 acccccccaa cacaaa 136

<210> 577
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 acccccccaa cacaaa 136

<210> 578
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<220>
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 acccccccaa cacaaa 136

<210> 580
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<220>
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 acccccccaa cacaaa 136

<210> 581
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<220>
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 acccccccaa cacaaa 136

<210> 582
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<220>
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 conserved sequence in 3' untranslated region

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 gacccccca acacaaa 137

<210> 583
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<220>
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 conserved sequence in 3' untranslated region

<400> 583
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 acccccccaa cacaaa 136

<210> 584
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<220>
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 conserved sequence in 3' untranslated region

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 acccccccaa cacaaa 136

<210> 585
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 <220>
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 conserved sequence in 3' untranslated region

 <400> 585
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 acccccccaa cacaaa 136

 <210> 586
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 conserved sequence in 3' untranslated region

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 gaccccccca acacaa 136

 <210> 587
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 acccccccaa cacaaa 136

 <210> 588
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 acccccccaa cacaaa 136

 <210> 589
 <211> 136
 <212> DNA
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<220>
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 acccccccaa cacaaa 136

<210> 590
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<220>
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 acccccccaa cacaaa 136

<210> 591
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<220>
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 acccccccaa cacaaa 136

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<220>
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<210> 593
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<220>
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 acccccccaa cacaa 135

<210> 594
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<220>
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<210> 595
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 acccccccaa cacaaa 136

<210> 596
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<220>
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 conserved sequence in 3' untranslated region

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<210> 597
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<210> 598
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conserved sequence in 3' untranslated region

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<210> 599
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conserved sequence in 3' untranslated region

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acccccccaa cacaaa 136

<210> 600
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<212> DNA
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<220>
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conserved sequence in 3' untranslated region

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acccccccaa cacaaa 136

<210> 601
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<213> Dengue virus type 4

<220>
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conserved sequence in 3' untranslated region

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agggggcccg aagccaggag gaagctgtac tcctggtgga aggactagag gttagaggag 120
acccccccaa cacaaa 136

<210> 602
<211> 136
<212> DNA
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<220>
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<210> 603
 <211> 136
 <212> DNA
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<220>
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 acccccccaa cacaaa 136

<210> 604
 <211> 136
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<220>
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 acccccccaa cacaaa 136

<210> 605
 <211> 137
 <212> DNA
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<220>
 <223> Dengue virus type 4 strain VR217-1 region of conserved sequence in 3' untranslated region

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 gacccccca acacaaa 137

<210> 606
 <211> 25
 <212> DNA
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<220>
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<400> 606
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 <210> 607
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
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 region of the genome of West Nile virus AF196835

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 <210> 608
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of West Nile virus AF260967

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 <210> 609
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF260968

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 <210> 610
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF260969

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 <210> 611
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 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF481864

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 <212> DNA
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 <220>
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 region of the genome of West Nile virus M12294

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 <210> 613
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 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF206518

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 <210> 614
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 <212> DNA
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 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of West Nile virus AF317203

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 <210> 615
 <211> 25
 <212> DNA
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 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of West Nile virus AF202541

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 <210> 616
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 <212> DNA
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 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of West Nile virus AF404757

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 <210> 617
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> region of conserved sequence in 3' untranslated
 region of the genome of West Nile virus AF404753

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 <210> 618
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF404754

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 <210> 619
 <211> 25
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 <220>
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 region of the genome of West Nile virus AF404755

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 <210> 620
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 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF404756

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 <210> 621
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF017254

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 <210> 622
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus L48977

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 <210> 623
 <211> 25
 <212> DNA
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 <220>
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 region of the genome of West Nile virus AF196536

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 <210> 624
 <211> 25
 <212> DNA
 <213> Artificial Sequence

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